

SEQUENCE LISTING

<110> Langenfeld, John

<120> BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CANCER

<130> 54704.8036.US03

<150> US60/261,252

<151> 2001-01-12

<150> US10/044,716

<151> 2002-01-11

<160> 20

<170> PatentIn version 3.2

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<223> Region: TGF-beta propeptide

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<221> variation

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 tgccccacac tgagacgctg ttcccagcgt gaaaagagag actgcgcggc cggcacccgg 180
 gagaaggagg aggcaaagaa aaggaacgga cattcggtcc ttgcgccagg tccttgacc 240
 agagttttc catgtggacg ctcttcaat ggacgtgtcc cgcgtgcctt cttagacgga 300
 ctgcggtctc ctaaaggctcg acc atg gtg gcc ggg acc cgc tgt ctt cta gcg 353
 Met Val Ala Gly Thr Arg Cys Leu Leu Ala
 1 5 10
 ttg ctg ctt ccc cag gtc ctc ctg ggc ggc gcg gct ggc ctc gtt ccg 401
 Leu Leu Leu Pro Gln Val Leu Leu Gly Ala Ala Gly Leu Val Pro
 15 20 25
 gag ctg ggc cgc agg aag ttc gcg gcg tcg tcg ggc cgc ccc tca 449
 Glu Leu Gly Arg Arg Lys Phe Ala Ala Ser Ser Gly Arg Pro Ser
 30 35 40
 tcc cag ccc tct gac gag gtc ctg agc gag ttc gag ttg cgg ctg ctc 497
 Ser Gln Pro Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu
 45 50 55
 agc atg ttc ggc ctg aaa cag aga ccc acc ccc agc agg gac gcc gtg 545
 Ser Met Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val
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 gtg ccc ccc tac atg cta gac ctg tat cgc agg cac tca ggt cag ccg 593
 Val Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro
 75 80 85 90
 ggc tca ccc gcc cca gac cac cgg ttg gag agg gca gcc agc cga gcc 641
 Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala
 95 100 105
 aac act gtg cgc agc ttc cac cat gaa gaa tct ttg gaa gaa cta cca 689
 Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro
 110 115 120
 gaa acg agt ggg aaa aca acc cgg aga ttc ttc ttt aat tta agt tct 737
 Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Asn Leu Ser Ser

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gaa cag atg caa gat gct tta gga aac aat agc agt ttc cat cac cga Glu Gln Met Gln Asp Ala Leu Gly Asn Asn Ser Ser Phe His His Arg 155	160	165	833
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ccc gtg acc aga ctt ttg gac acc agg ttg gtg aat cag aat gca agc Pro Val Thr Arg Leu Leu Asp Thr Arg Leu Val Asn Gln Asn Ala Ser 190	195	200	929
agg tgg gaa agt ttt gat gtc acc ccc gct gtg atg cgg tgg act gca Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val Met Arg Trp Thr Ala 205	210	215	977
cag gga cac gcc aac cat gga ttc gtg gtg gaa gtg gcc cac ttg gag Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His Leu Glu 220	225	230	1025
gag aaa caa ggt gtc tcc aag aga cat gtt agg ata agc agg tct ttg Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu 235	240	245	1073
cac caa gat gaa cac agc tgg tca cag ata agg cca ttg cta gta act His Gln Asp Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr 255	260	265	1121
ttt ggc cat gat gga aaa ggg cat cct ctc cac aaa aga gaa aaa cgt Phe Gly His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg 270	275	280	1169
caa gcc aaa cac aaa cag cgg aaa cgc ctt aag tcc agc tgt aag aga Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg 285	290	295	1217
cac cct ttg tac gtg gac ttc agt gac gtg ggg tgg aat gac tgg att His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile 300	305	310	1265
gtg gct ccc ccc ggg tat cac gcc ttt tac tgc cac gga gaa tgc cct Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro 315	320	325	1313
ttt cct ctg gct gat cat ctg aac tcc act aat cat gcc att gtt cag Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln 335	340	345	1361
acg ttg gtc aac tct gtt aac tct aag att cct aag gca tgc tgt gtc Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val 350	355	360	1409

ccg aca gaa ctc agt gct atc tcg atg ctg tac ctt gac gag aat gaa 1457
 Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
 365 370 375

aag gtt gta tta aag aac tat cag gac atg gtt gtg gag ggt tgt ggg 1505
 Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
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Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
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Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
 50 55 60

Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
 65 70 75 80

Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
 85 90 95

His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
 100 105 110

His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
 115 120 125

Thr Arg Arg Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
 130 135 140

Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
 145 150 155 160

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
 165 170 175

Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
 180 185 190

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
 195 200 205

Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
 210 215 220

Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
 225 230 235 240

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
 245 250 255

Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
 260 265 270

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
 275 280 285

Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 290 295 300

Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
 305 310 315 320

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
 325 330 335

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
 340 345 350

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
 355 360 365

Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn

<302> TGF beta inhibitors. New and unexpected requirements in
 vertebrate development
 <303> Trends Genet.
 <304> 15
 <305> 1
 <306> 3-5
 <307> 1999
 <308> NM_005450
 <309> 2000-11-01
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<300>
 <301> Gong,Y., Krakow,D., Marcelino,J., Wilkin,D., Chitayat,D.,
 Babul-Hirji,R., Hudgins,L., Cremers,C.W., Cremers,F.P.,
 Brunner,H.G., Reinker,K., Rimoin,D.L., Cohn,D.H., Goodman,F.R.,
 Reardon,W., Patton,M., Francomano,C.A. and Warman,M.L.
 <302> Heterozygous mutations in the gene encoding noggin affect human
 joint morphogenesis
 <303> Nat. Genet.
 <304> 21
 <305> 3
 <306> 302-304
 <307> 1999
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 Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
 20 25 30

atc cgc ccg gca ccc agc gac aac ctg ccc ctg gtg gac ctc atc gaa 144

Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu			
35	40	45	
cac cca gac cct atc ttt gac ccc aag gaa aag gat ctg aac gag acg			192
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr			
50	55	60	
ctg ctg cgc tcg ctc ggg ggc cac tac gac cca ggc ttc atg gcc			240
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala			
65	70	75	80
acc tcg ccc ccc gag gac cgg ccc ggc ggg ggc ggg ggt gca gct ggg			288
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Ala Ala Gly			
85	90	95	
ggc gcg gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg			336
Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro			
100	105	110	
tcg ggg gcc atg ccg agc gag atc aaa ggg cta gag ttc tcc gag ggc			384
Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly			
115	120	125	
ttg gcc cag ggc aag aag cag cgc cta agc aag aag ctg cgg agg aag			432
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys			
130	135	140	
tta cag atg tgg ctg tgg tcg cag aca ttc tgc ccc gtg ctg tac gcg			480
Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala			
145	150	155	160
tgg aac gac ctg ggc agc cgc ttt tgg ccg cgc tac gtg aag gtg ggc			528
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly			
165	170	175	
agc tgc ttc agt aag cgc tcg tgc tcc gtg ccc gag ggc atg gtg tgc			576
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys			
180	185	190	
aag ccg tcc aag tcc gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag			624
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln			
195	200	205	
cg _g cgc ggg ggc cag cgc tgc ggc tgg att ccc atc cag tac ccc atc			672
Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile			
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Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu
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His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr
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Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala
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Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Ala	Ala	Gly	
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130															135

Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala
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Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys
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Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln
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Arg	Arg	Gly	Gly	Gln	Arg	Cys	Gly	Trp	Ile	Pro	Ile	Gln	Tyr	Pro	Ile
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 Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
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 Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
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His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
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 Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
 85 90 95

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Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
100          105          110

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ttg gcc caa ggc aag aaa cag cgc ctg agc aag aag ctg agg agg agg aag 432
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
    130           135           140

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145 150 155 160	
tgg aat gac cta ggc agc cgc ttt tgg cca cgc tac gtg aag gtg ggc	528
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly	
165 170 175	
agc tgc ttc agc aag cgc tcc tgc tct gtg ccc gag ggc atg gtg tgt	576
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys	
180 185 190	
aag cca tcc aag tct gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag	624
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln	
195 200 205	
cgg cgc ggg ggt cag cgc tgc ggc tgg att ccc atc cag tac ccc atc	672
Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile	
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Ile Ser Glu Cys Lys Cys Ser Cys	
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His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr	
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Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
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Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
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Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
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Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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 <301> Millet, C., Lemaire, P., Orsetti, B., Guglielmi, P., and
 Francois, V.
 <302> The human chordin gene encodes several differentially expressed
 spliced variants with distinct BMP opposing activities
 <303> Mech. Dev.
 <304> 106
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 <306> 85-96
 <307> 2001
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 <301> Millet, C., and Francois, V.

<302> Direct Submission
<303> Institut de Genetique Humaine
<304> 1
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<307> 1999-11-30
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tgt ggg cag ccg cgc cag ctg ccg gga cac tgc tgc cag acc tgc ccc Cys Gly Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro			624
115 120 125			
cag gag cgc agc agt tcg gag cgg cag ccg agc ggc ctg tcc ttc gag Gln Glu Arg Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu			672
130 135 140			
tat ccg cgg gac ccg gag cat cgc agt tat agc gac cgc ggg gag cca Tyr Pro Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro			720
145 150 155			
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160 165 170			
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175 180 185 190			
ctg ctg cgc tct agc ctc cgc ttc tct atc tcc tac agg cgg ctg gac Leu Leu Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp			864
195 200 205			
cgc cct acc agg atc cgc ttc tca gac tcc aat ggc agt gtc ctg ttt Arg Pro Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe			912
210 215 220			
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225 230 235			
cgg gca gtg cct cgg ttg tct ctg cgg ctc ctt agg gca gaa cag ctg Arg Ala Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu			1008
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305 310 315			

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agg ctc cag att cta cac cag ggg cag cta ctg cga gaa ctt cag gcc Arg Leu Gln Ile Leu His Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala 335 340 345 350	1296
aat gtc tca gcc cag gaa cca ggc ttt gct gag gtg ctg ccc aac ctg Asn Val Ser Ala Gln Glu Pro Gly Phe Ala Glu Val Leu Pro Asn Leu 355 360 365	1344
aca gtc cag gag atg gac tgg ctg gtg ctg ggg gag ctg cag atg gcc Thr Val Gln Glu Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala 370 375 380	1392
ctg gag tgg gca ggc agg cca ggg ctg cgc atc agt gga cac att gct Leu Glu Trp Ala Gly Arg Pro Gly Leu Arg Ile Ser Gly His Ile Ala 385 390 395	1440
gcc agg aag agc tgc gac gtc ctg caa agt gtc ctt tgt ggg gct gat Ala Arg Lys Ser Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp 400 405 410	1488
gcc ctg atc cca gtc cag acg ggt gct gcc ggc tca gcc agc ctc acg Ala Leu Ile Pro Val Gln Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr 415 420 425 430	1536
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Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala Gly Thr Arg		
785	790	795
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Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys Cys Ala Val Cys		
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Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys Glu Lys Val Gln Cys		
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Pro Arg Leu Ala Cys Ala Gln Pro Val Arg Val Asn Pro Thr Asp Cys		
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Cys Lys Gln Cys Pro Val Gly Ser Gly Ala His Pro Gln Leu Gly Asp		
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Pro Met Gln Ala Asp Gly Pro Arg Gly Cys Arg Phe Ala Gly Gln Trp		
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Phe Pro Glu Ser Gln Ser Trp His Pro Ser Val Pro Pro Phe Gly Glu		
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His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys			
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Val Ser Cys Lys Asn Ile Lys Pro Glu Cys Pro Thr Pro Ala Cys Gly		
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Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu		
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Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala			
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Glu Glu Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu		
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Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro
 195 200 205

Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His
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Pro Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
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Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His Val
 245 250 255

Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu
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Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr
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Gln Glu Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala Leu Glu
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Lys Ser Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu
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Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met Leu
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Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys Gly His Ser
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Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly Ala Leu Val Leu
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Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala Trp Leu Ser Leu Asp
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Thr His Cys His Leu His Tyr Glu Val Leu Leu Ala Gly Leu Gly Gly
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Ser Glu Gln Gly Thr Val Thr Ala His Leu Leu Gly Pro Pro Gly Thr
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Ala Pro Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr			
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Cys Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro			
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770	775	780	
Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala Gly Thr Arg Trp His			
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Pro Val Val Pro Pro Phe Gly Leu Ile Lys Cys Ala Val Cys Thr Cys			
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Lys Gly Gly Thr Gly Glu Val His Cys Glu Lys Val Gln Cys Pro Arg			
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Leu Ala Cys Ala Gln Pro Val Arg Val Asn Pro Thr Asp Cys Cys Lys			
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Gln Cys Pro Val Gly Ser Gly Ala His Pro Gln Leu Gly Asp Pro Met			
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Gln Ala Asp Gly Pro Arg Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro
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Glu Ser Gln Ser Trp His Pro Ser Val Pro Pro Phe Gly Glu Met Ser
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Cys Ile Thr Cys Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp
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      Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu
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Leu Gly Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln
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ggt gcc atc ccc ccg cca gac aag gcc cag cac aat gac tca gag cag      267
Gly Ala Ile Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln
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act cag tcg ccc cag cag cct ggc tcc agg aac cgg ggg cgg ggc caa      315
Thr Gln Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln
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ggg cgg ggc act gcc atg ccc ggg gag gag gtg ctg gag tcc agc caa      363
Gly Arg Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln
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gag gcc ctg cat gtg acg gag cgc aaa tac ctg aag cga gac tgg tgc      411
Glu Ala Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys
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aaa acc cag ccg ctt aag cag acc atc cac gag gaa ggc tgc aac agt      459
Lys Thr Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser
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cgc acc atc atc aac cgc ttc tgt tac ggc cag tgc aac tct ttc tac      507
Arg Thr Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr
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atc ccc agg cac atc cgg aag gag gaa ggt tcc ttt cag tcc tgc tcc      555
Ile Pro Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser
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ttc tgc aag ccc aag aaa ttc act acc atg atg gtc aca ctc aac tgc      603

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Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr
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Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro
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Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys
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 Harvey, R.P.
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 Val Leu Pro Arg Asn Gln Arg Glu Leu Pro Thr Gly Asn His Glu
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gaa gct gag gag aag cca gat ctg ttt gtc gca gtg cca cac ctt gta 192
 Glu Ala Glu Glu Lys Pro Asp Leu Phe Val Ala Val Pro His Leu Val
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gcc acc agc cct gca ggg gaa ggc cag agg cag aga gag aag atg ctg 240
 Ala Thr Ser Pro Ala Gly Glu Gly Gln Arg Gln Arg Glu Lys Met Leu
 65 70 75 80

tcc aga ttt ggc agg ttc tgg aag aag cct gag aga gaa atg cat cca 288
 Ser Arg Phe Gly Arg Phe Trp Lys Lys Pro Glu Arg Glu Met His Pro
 85 90 95

tcc agg gac tca gat agt gag ccc ttc cca cct ggg acc cag tcc ctc	336
Ser Arg Asp Ser Asp Ser Glu Pro Phe Pro Pro Gly Thr Gln Ser Leu	
100 105 110	
atc cag ccg ata gat gga atg aaa atg gag aaa tct cct ctt ccg gaa	384
Ile Gln Pro Ile Asp Gly Met Lys Met Glu Lys Ser Pro Leu Arg Glu	
115 120 125	
gaa gcc aag aaa ttc tgg cac cac ttc atg ttc aga aaa act ccg gct	432
Glu Ala Lys Lys Phe Trp His His Phe Met Phe Arg Lys Thr Pro Ala	
130 135 140	
tct cag ggg gtc atc ttg ccc atc aaa agc cat gaa gta cat tgg gag	480
Ser Gln Gly Val Ile Leu Pro Ile Lys Ser His Glu Val His Trp Glu	
145 150 155 160	
acc tgc agg aca gtg ccc ttc agc cag act ata acc cac gaa ggc tgt	528
Thr Cys Arg Thr Val Pro Phe Ser Gln Thr Ile Thr His Glu Gly Cys	
165 170 175	
gaa aaa gta gtt gtt cag aac aac ctt tgc ttt ggg aaa tgc ggg tct	576
Glu Lys Val Val Val Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser	
180 185 190	
gtt cat ttt cct gga gcc gcg cag cac tcc cat acc tcc tgc tct cac	624
Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His	
195 200 205	
tgt ttg cct gcc aag ttc acc acg atg cac ttg cca ctg aac tgc act	672
Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr	
210 215 220	
gaa ctt tcc tcc gtg atc aag gtg gtg atg ctg gtg gag gag tgc cag	720
Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln	
225 230 235 240	
tgc aag gtg aag acg gag cat gaa gat gga cac atc cta cat gct ggc	768
Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly	
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tcc cag gat tcc ttt atc cca gga gtt tca gct tga	804
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Val Leu Leu Pro Arg Asn Gln Arg Glu Leu Pro Thr Gly Asn His Glu
 35 40 45

Glu Ala Glu Glu Lys Pro Asp Leu Phe Val Ala Val Pro His Leu Val
 50 55 60

Ala Thr Ser Pro Ala Gly Glu Gly Gln Arg Gln Arg Glu Lys Met Leu
 65 70 75 80

Ser Arg Phe Gly Arg Phe Trp Lys Lys Pro Glu Arg Glu Met His Pro
 85 90 95

Ser Arg Asp Ser Asp Ser Glu Pro Phe Pro Pro Gly Thr Gln Ser Leu
 100 105 110

Ile Gln Pro Ile Asp Gly Met Lys Met Glu Lys Ser Pro Leu Arg Glu
 115 120 125

Glu Ala Lys Lys Phe Trp His His Phe Met Phe Arg Lys Thr Pro Ala
 130 135 140

Ser Gln Gly Val Ile Leu Pro Ile Lys Ser His Glu Val His Trp Glu
 145 150 155 160

Thr Cys Arg Thr Val Pro Phe Ser Gln Thr Ile Thr His Glu Gly Cys
 165 170 175

Glu Lys Val Val Val Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser
 180 185 190

Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His
 195 200 205

Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr
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Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln
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Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly

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 <301> ten Dijke, P., Yamashita, H., Ichijo, H., Franzen, P., Laiho, M., Miyazono, K., and Heldin, C.H.
 <302> Characterization of type I receptors for transforming growth factor-beta and activin
 <303> Science
 <304> 264
 <305> 5155
 <306> 101-104
 <307> 1994
 <308> NM_001203
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 <301> Ide, H., Katoh, M., Sasaki, H., Yoshida, T., Aoki, K., Nawa, Y., Osada, Y., Sugimura, T., and Terada, M.
 <302> Cloning of human bone morphogenetic protein type IB receptor (BMPR-IB) and its expression in prostate cancer in comparison with other BMPRs
 <303> Oncogene
 <304> 14
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 <306> 1377-1382
 <307> 1997
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 <301> Ide, H., Saito-Ohara, P., Ohnami, S., Osada, Y., Ikeuchi, T., Yoshida, T., and Terada, M.
 <302> Assignment of the BMPR1A and BMPR1B genes to human chromosome 10q22.3 and 4q23-->q24 by in situ hybridization and radiation hybrid mapping
 <303> Cytogenet. Cell. Genet.
 <304> 81
 <305> 3
 <306> 285-286
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 <309> 2000-10-31
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<301> Astrom, A.K., Jin, D., Imamura, T., Roijer, E., Rosenzweig, B.,
 Miyazono, K., ten Dijke, P., and Stenman, G.
 <302> Chromosomal localization of three human genes encoding bone
 morphogenetic protein receptors
 <303> Mamm. Genome
 <304> 10
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 gtgaaaaggaa aggaagatca tttcatgcct tggataaa gttcagact tctgctgatt 180
 cataaccatt tggctctgag ctatgacaag agagaaaaca aaaagttaaa cttacaagcc 240

tgccataagt gagaagcaaa cttccttgat aac atg ctt ttg cga agt gca gga 294
 Met Leu Leu Arg Ser Ala Gly
 1 5
 aaa tta aat gtg ggc acc aag aaa gag gat ggt gag agt aca gcc ccc 342
 Lys Leu Asn Val Gly Thr Lys Lys Glu Asp Gly Glu Ser Thr Ala Pro
 10 15 20
 acc ccc cgt cca aag gtc ttg cgt tgt aaa tgc cac cac cat tgt cca 390
 Thr Pro Arg Pro Lys Val Leu Arg Cys Lys Cys His His His Cys Pro
 25 30 35
 gaa gac tca gtc aac aat att tgc agc aca gac gga tat tgt ttc acg 438
 Glu Asp Ser Val Asn Asn Ile Cys Ser Thr Asp Gly Tyr Cys Phe Thr
 40 45 50 55
 atg ata gaa gag gat gac tct ggg ttg cct gtg gtc act tct ggt tgc 486
 Met Ile Glu Glu Asp Asp Ser Gly Leu Pro Val Val Thr Ser Gly Cys
 60 65 70
 cta gga cta gaa ggc tca gat ttt cag tgt cgg gac act ccc att cct 534
 Leu Gly Leu Glu Gly Ser Asp Phe Gln Cys Arg Asp Thr Pro Ile Pro
 75 80 85
 cat caa aga aga tca att gaa tgc tgc aca gaa agg aac gaa tgt aat 582
 His Gln Arg Arg Ser Ile Glu Cys Cys Thr Glu Arg Asn Glu Cys Asn
 90 95 100
 aaa gac cta cac cct aca ctg cct cca ttg aaa aac aga gat ttt gtt 630
 Lys Asp Leu His Pro Thr Leu Pro Pro Leu Lys Asn Arg Asp Phe Val
 105 110 115
 gat gga cct ata cac cac agg gct tta ctt ata tct gtg act gtc tgt 678
 Asp Gly Pro Ile His His Arg Ala Leu Leu Ile Ser Val Thr Val Cys
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 Ser Leu Leu Leu Val Leu Ile Ile Leu Phe Cys Tyr Phe Arg Tyr Lys
 140 145 150
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 Arg Gln Glu Thr Arg Pro Arg Tyr Ser Ile Gly Leu Glu Gln Asp Glu
 155 160 165
 act tac att cct cct gga gaa tcc ctg aga gac tta att gag cag tct 822
 Thr Tyr Ile Pro Pro Gly Glu Ser Leu Arg Asp Leu Ile Glu Gln Ser
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 cag agc tca gga agt gga tca ggc ctc cct ctg gtc caa agg act 870
 Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr
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 Ile Ala Lys Gln Ile Gln Met Val Lys Gln Ile Gly Lys Gly Arg Tyr
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tat cag aca gtg ttg atg agg cat gaa aac att ttg ggt ttc att gct Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala 250 255 260	1062
gca gat atc aaa ggg aca ggg tcc tgg acc cag ttg tac cta atc aca Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr 265 270 275	1110
gac tat cat gaa aat ggt tcc ctt tat gat tat ctg aag tcc acc acc Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Tyr Leu Lys Ser Thr Thr 280 285 290 295	1158
cta gac gct aaa tca atg ctg aag tta gcc tac tct tct gtc agt ggc Leu Asp Ala Lys Ser Met Leu Lys Leu Ala Tyr Ser Ser Val Ser Gly 300 305 310	1206
tta tgt cat tta cac aca gaa atc ttt agt act caa ggc aaa cca gca Leu Cys His Leu His Thr Glu Ile Phe Ser Thr Gln Gly Lys Pro Ala 315 320 325	1254
att gcc cat cga gat ctg aaa agt aaa aac att ctg gtc aag aaa aat Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn 330 335 340	1302
gga act tgc tgt att gct gac ctg ggc ctg gct gtt aaa ttt att agt Gly Thr Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Ile Ser 345 350 355	1350
gat aca aat gaa gtt gac ata cca cct aac act cga gtt ggc acc aaa Asp Thr Asn Glu Val Asp Ile Pro Pro Asn Thr Arg Val Gly Thr Lys 360 365 370 375	1398
cgc tat atg cct cca gaa gtg ttg gac gag agc ttg aac aga aat cac Arg Tyr Met Pro Pro Glu Val Leu Asp Glu Ser Leu Asn Arg Asn His 380 385 390	1446
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Met Arg Glu Ile Val Cys Ile Lys Lys Leu Arg Pro Ser Phe Pro Asn			
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cgg tgg agc agt gat gag tgt cta agg cag atg gga aaa ctc atg aca			1686
Arg Trp Ser Ser Asp Glu Cys Leu Arg Gln Met Gly Lys Leu Met Thr			
460	465	470	
gaa tgc tgg gct cac aat cct gca tca agg ctg aca gcc ctg cgg gtt			1734
Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu Thr Ala Leu Arg Val			
475	480	485	
aag aaa aca ctt gcc aaa atg tca gag tcc cag gac att aaa ctc tga			1782
Lys Lys Thr Leu Ala Lys Met Ser Glu Ser Gln Asp Ile Lys Leu			
490	495	500	
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Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser			
35	40	45	

Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Leu			
50	55	60	

Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln			
65	70	75	80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys			
85	90	95	

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110

Leu Lys Asn Arg Asp Phe Val Asp Gly Pro Ile His His Arg Ala Leu
 115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Thr Arg Pro Arg Tyr Ser
 145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
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Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
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Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys

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330

335

Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
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Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
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Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
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